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OIIPE

RAW SEQUENCE LISTING

DATE: 11/14/2001

PATENT APPLICATION: US/09/943,108

TIME: 15:44:16

Input Set : N:\Crf3\RULE60\09943108.txt

Output Set: N:\CRF3\11142001\I943108.raw

4 <110> APPLICANT: Black, Michael T.
7 <120> TITLE OF INVENTION: SIGNAL RECOGNITION PARTICLE POLYPEPTIDES
8 AND POLYNUCLEOTIDES
10 <130> FILE REFERENCE: GM50035
12 <140> CURRENT APPLICATION NUMBER: 09/943,108
13 <141> CURRENT FILING DATE: 2001-08-30
15 <150> PRIOR APPLICATION NUMBER: 09/035,382
16 <151> PRIOR FILING DATE: 1998-03-05
18 <160> NUMBER OF SEQ ID NOS: 8
20 <170> SOFTWARE: FastSEQ for Windows Version 3.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1368
24 <212> TYPE: DNA
25 <213> ORGANISM: Staphylococcus aureus
27 <400> SEQUENCE: 1

28	atggcatttg	aaggcttatt	agaacgcctg	caagcgacga	tgcaaaaaat	gcgtggtaag	60
29	ggtaaactta	ctgaagctga	tataaagata	atgatgcgtg	aagtaagatt	agcgttattt	120
30	gaggctgacg	taaacttta	agtggtaaaa	gaatttatta	aaacagtatc	agaacgcgca	180
31	ttaggttccg	atgtaatgca	atcattaaca	ccaggggcaac	aagttattaa	aatagttcaa	240
32	gatgaattaa	cgaagttgat	gggtggagaa	aatacatcga	ttaatatgtc	aaataaacca	300
33	cctactgttg	ttatgatggt	tggtttacaa	ggtgctggta	aaacaacaac	tcgaggtaaa	360
34	ttagcattat	tgatgcgtaa	aaaatacaac	aaaaaaccta	tgtagttgac	agcagatatt	420
35	tatcgtccag	cagcgataaa	tcaattacaa	acagtaggga	aacaaattga	tattcctgta	480
36	tacagtgaag	gagatcaagt	aaagccacaa	caaattgtaa	ctaattgcatt	aaaacatgct	540
37	aaagaagaac	atttagactt	tgtaatcatt	gatacagcag	gtcgattaca	catcgatgaa	600
38	gcattgatga	acgaattaaa	agaagtaaaa	gaaattgcta	aaccaaacga	aattatgtta	660
39	gttgctcgatt	caatgacggg	tcaagatgct	gtcaatgttg	cagaatcttt	tgacgatcaa	720
40	cttgatgtca	cagggtgttac	cttaactaaa	ttagatgggt	atacacgtgg	tggtgcagct	780
41	ttatctattc	gttcggtgac	acaaaaacca	attaaatttg	ttggtatgag	tgaaaagtta	840
42	gatgggttag	agctattcca	tcctgaacgt	atggcatcac	gtatttttag	tatgggtgat	900
43	gtgttaagtt	taattgaaaa	agcgcaacaa	gatgtggatc	aagaaaaagc	aaaagattta	960
44	gagaaaaaga	tgctgagtc	atcgtttact	ttagatgatt	ttttagaaca	acttgatcag	1020
45	gtgaaaaatc	taggaccact	ggatgatatt	atgaaaatga	ttccagggtat	gaataaaatg	1080
46	aaagggttag	ataagcttaa	tatgagtga	aagcaaattg	atcatattaa	agcgattatc	1140
47	cagtcaatga	cgccggctga	aagaaacaat	ccagacacat	tgaatgtatc	acgtaaaaag	1200
48	cgtattgcta	aagggtctgg	tcgttcatta	caagaagtca	atcgtttgat	gaaacaattt	1260
49	aacgatatga	agaaaatgat	gaaacaattc	actggtggcg	gtaaaggtaa	aaaaggtaaa	1320
50	cgcaatcaaa	tgcaaaatat	gttaaaaggt	atgaatttac	cgttttaa		1368

52 <210> SEQ ID NO: 2
53 <211> LENGTH: 455
54 <212> TYPE: PRT
55 <213> ORGANISM: Staphylococcus aureus
57 <400> SEQUENCE: 2

58	Met	Ala	Phe	Glu	Leu	Ser	Glu	Arg	Leu	Gln	Ala	Thr	Met	Gln	Lys
59	1			5				10						15	
60	Met	Arg	Gly	Lys	Gly	Lys	Leu	Thr	Glu	Ala	Asp	Ile	Lys	Ile	Met
61				20				25						30	

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62 Arg Glu Val Arg Leu Ala Leu Phe Glu Ala Asp Val Asn Phe Lys Val
63      35      40      45
64 Val Lys Glu Phe Ile Lys Thr Val Ser Glu Arg Ala Leu Gly Ser Asp
65      50      55      60
66 Val Met Gln Ser Leu Thr Pro Gly Gln Gln Val Ile Lys Ile Val Gln
67      65      70      75      80
68 Asp Glu Leu Thr Lys Leu Met Gly Gly Glu Asn Thr Ser Ile Asn Met
69      85      90      95
70 Ser Asn Lys Pro Pro Thr Val Val Met Met Val Gly Leu Gln Gly Ala
71      100      105      110
72 Gly Lys Thr Thr Ala Gly Lys Leu Ala Leu Leu Met Arg Lys Lys
73      115      120      125
74 Tyr Asn Lys Lys Pro Met Leu Val Ala Ala Asp Ile Tyr Arg Pro Ala
75      130      135      140
76 Ala Ile Asn Gln Leu Gln Thr Val Gly Lys Gln Ile Asp Ile Pro Val
77      145      150      155      160
78 Tyr Ser Glu Gly Asp Gln Val Lys Pro Gln Gln Ile Val Thr Asn Ala
79      165      170      175
80 Leu Lys His Ala Lys Glu Glu His Leu Asp Phe Val Ile Ile Asp Thr
81      180      185      190
82 Ala Gly Arg Leu His Ile Asp Glu Ala Leu Met Asn Glu Leu Lys Glu
83      195      200      205
84 Val Lys Glu Ile Ala Lys Pro Asn Glu Ile Met Leu Val Val Asp Ser
85      210      215      220
86 Met Thr Gly Gln Asp Ala Val Asn Val Ala Glu Ser Phe Asp Asp Gln
87      225      230      235      240
88 Leu Asp Val Thr Gly Val Thr Leu Thr Lys Leu Asp Gly Asp Thr Arg
89      245      250      255
90 Gly Gly Ala Ala Leu Ser Ile Arg Ser Val Thr Gln Lys Pro Ile Lys
91      260      265      270
92 Phe Val Gly Met Ser Glu Lys Leu Asp Gly Leu Glu Leu Phe His Pro
93      275      280      285
94 Glu Arg Met Ala Ser Arg Ile Leu Gly Met Gly Asp Val Leu Ser Leu
95      290      295      300
96 Ile Glu Lys Ala Gln Gln Asp Val Asp Gln Glu Lys Ala Lys Asp Leu
97      305      310      315      320
98 Glu Lys Lys Met Arg Glu Ser Ser Phe Thr Leu Asp Asp Phe Leu Glu
99      325      330      335
100 Gln Leu Asp Gln Val Lys Asn Leu Gly Pro Leu Asp Asp Ile Met Lys
101      340      345      350
102 Met Ile Pro Gly Met Asn Lys Met Lys Gly Leu Asp Lys Leu Asn Met
103      355      360      365
104 Ser Glu Lys Gln Ile Asp His Ile Lys Ala Ile Ile Gln Ser Met Thr
105      370      375      380
106 Pro Ala Glu Arg Asn Asn Pro Asp Thr Leu Asn Val Ser Arg Lys Lys
107      385      390      395      400
108 Arg Ile Ala Lys Gly Ser Gly Arg Ser Leu Gln Glu Val Asn Arg Leu
109      405      410      415
110 Met Lys Gln Phe Asn Asp Met Lys Lys Met Met Lys Gln Phe Thr Gly

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111          420          425          430
112 Gly Gly Lys Gly Lys Lys Gly Lys Arg Asn Gln Met Gln Asn Met Leu
113          435          440          445
114 Lys Gly Met Asn Leu Pro Phe
115          450          455
117 <210> SEQ ID NO: 3
118 <211> LENGTH: 792
119 <212> TYPE: DNA
120 <213> ORGANISM: Staphylococcus aureus
122 <400> SEQUENCE: 3
123 atggcatttg aaggcttatc agaacgcctg caagcgacga tgcaaaaaat gcgtggttaag      60
124 ggtaaaactta ctgaagctga tataaagata atgatgcgtg aagtaagatt agcgttatatt      120
125 gaggtgacg taaactttaa agtggtaaaa gaatttatta aaacagtatc agaacgcgca      180
126 ttaggttccg atgtaatgca atcattaaca ccagggcaac aagttattaa aatagttcaa      240
127 gatgaattaa cgaagttgat ggggtggagaa aatacatcga ttaatatgtc aaataaacca      300
128 cctactgttg ttatgatggt tggtttacaa ggtgctggtg aaacaacaac tgcaggtaaa      360
129 ttagcattat tgatgcgtaa aaaatacaac aaaaaacctg tgttagttgc agcagatatt      420
130 tatcgtccag cagcgataaa tcaattacaa acagtaggga aacaaattga tattcctgta      480
131 tacagtgaag gagatcaagt aaagccacaa caaattgtaa ctaatgcatt aaaacatgct      540
132 aaagaagaac atttagactt tgtaatcatt gatacagcag gtcgattaca catcgatgaa      600
133 gcattgatga acgaattaaa agaagtaaaa gaaattgcta aaccaaacga aattatgtta      660
134 gttgtcgatt caatgacggg tcaagatgct gtcaatgttg cagaatcttt tgacgatcaa      720
135 cttgatgtca caggtgttac cttaactaaa ttagatggtg ataccctggg tgggtcagct      780
136 ttatctattc gt                                     792
138 <210> SEQ ID NO: 4
139 <211> LENGTH: 264
140 <212> TYPE: PRT
141 <213> ORGANISM: Staphylococcus aureus
143 <400> SEQUENCE: 4
144 Met Ala Phe Glu Gly Leu Ser Glu Arg Leu Gln Ala Thr Met Gln Lys
145 1          5          10          15
146 Met Arg Gly Lys Gly Lys Leu Thr Glu Ala Asp Ile Lys Ile Met Met
147          20          25          30
148 Arg Glu Val Arg Leu Ala Leu Phe Glu Ala Asp Val Asn Phe Lys Val
149          35          40          45
150 Val Lys Glu Phe Ile Lys Thr Val Ser Glu Arg Ala Leu Gly Ser Asp
151          50          55          60
152 Val Met Gln Ser Leu Thr Pro Gly Gln Gln Val Ile Lys Ile Val Gln
153          65          70          75          80
154 Asp Glu Leu Thr Lys Leu Met Gly Gly Glu Asn Thr Ser Ile Asn Met
155          85          90          95
156 Ser Asn Lys Pro Pro Thr Val Val Met Met Val Gly Leu Gln Gly Ala
157          100         105         110
158 Gly Lys Thr Thr Thr Ala Gly Lys Leu Ala Leu Leu Met Arg Lys Lys
159          115         120         125
160 Tyr Asn Lys Lys Pro Met Leu Val Ala Ala Asp Ile Tyr Arg Pro Ala
161          130         135         140
162 Ala Ile Asn Gln Leu Gln Thr Val Gly Lys Gln Ile Asp Ile Pro Val
163          145         150         155         160

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164 Tyr Ser Glu Gly Asp Gln Val Lys Pro Gln Gln Ile Val Thr Asn Ala
165           165           170           175
166 Leu Lys His Ala Lys Glu Glu His Leu Asp Phe Val Ile Ile Asp Thr
167           180           185           190
168 Ala Gly Arg Leu His Ile Asp Glu Ala Leu Met Asn Glu Leu Lys Glu
169           195           200           205
170 Val Lys Glu Ile Ala Lys Pro Asn Glu Ile Met Leu Val Val Asp Ser
171           210           215           220
172 Met Thr Gly Gln Asp Ala Val Asn Val Ala Glu Ser Phe Asp Asp Gln
173           225           230           235           240
174 Leu Asp Val Thr Gly Val Thr Leu Thr Lys Leu Asp Gly Asp Thr Arg
175           245           250           255
176 Gly Gly Ala Ala Leu Ser Ile Arg
177           260
179 <210> SEQ ID NO: 5
180 <211> LENGTH: 500
181 <212> TYPE: DNA
182 <213> ORGANISM: Staphylococcus aureus
184 <400> SEQUENCE: 5
185 aaacatcttg caaatgaatt taaatttaac gacttctcaa gacgtcgtat aaagtaaaca      60
186 atgatataaa tgatttatac ttgcaattaa ctattaaaat atagtaatat atatcttgcc      120
187 gtgctagggtg gggaggtagc ggttccctgt actcgaaatc cgctttatgc gaggcttaat      180
188 tcctttgttg aggccgtatt tttgcgaagt ctgcccagg cagctagtgt ttgaagattt      240
189 cggtcctatg caatatgaac ccatagaacca tgtcagggtcc tgacggaagc agcattaagt      300
190 ggatcatcat atgtgccgta gggtagccga gatttagcta acgacttttg ttacgttcgt      360
191 gaattacgtt cgatgcttag gtgcacggtt ttttattttt taaatattaa accgattatt      420
192 aagagttgaa aatatatatt tatittataga agctactttc ttgaagacaa ttcagcgtat      480
193 tatacgtgga acatgtttgt
195 <210> SEQ ID NO: 6
196 <211> LENGTH: 358
197 <212> TYPE: DNA
198 <213> ORGANISM: Staphylococcus aureus
200 <400> SEQUENCE: 6
201 acttgcaatt aactattaaa atatagtaat atatatcttg ccgtgctagg tggggaggta      60
202 gcggttccct gtactcgaaa tccgctttat gcgaggctta attcctttgt tgaggccgta      120
203 tttttgcgaa gtctgcccaa agcacgtagt gtttgaagat ttcggtccta tgcaatatga      180
204 acccatgaac catgtcaggt cctgacggaa gcagcattaa gtggatcatc atatgtgccg      240
205 tagggtagcc gagatttagc taacgacttt ggttacgttc gtgaattacg ttcgatgctt      300
206 aggtgcacgg ttttttattt tttaaatatt aaaccgatta ttaagagttg aaaatata      358
208 <210> SEQ ID NO: 7
209 <211> LENGTH: 276
210 <212> TYPE: DNA
211 <213> ORGANISM: Staphylococcus aureus
213 <400> SEQUENCE: 7
214 cttgcctgac taggtgggga ggtagcgggt ccctgtactc gaaatccgct ttatgcgagg      60
215 cttaattcct ttgttgaggc cgtatttttt cgaagtctgc ccaaagcacg tagtgtttga      120
216 agatttcggt cctatgcaat atgaacccat gaaccatgtc aggtcctgac ggaagcagca      180
217 ttaagtggat catcatatgt gccgtagggt agccgagatt tagctaacga ctttggttac      240
218 gttcgtgaat tacgttcgat gcttaggtgc acggtt      276

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220 <210> SEQ ID NO: 8
221 <211> LENGTH: 275
222 <212> TYPE: DNA
223 <213> ORGANISM: Staphylococcus aureus
225 <220> FEATURE:
226 <221> NAME/KEY: misc_feature
227 <222> LOCATION: (1)...(275)
228 <223> OTHER INFORMATION: n = A,T,C or G
230 <400> SEQUENCE: 8
231 aacaatgccg tttcaatata atatttcaaa acatcttgca aatgaattta aatttaccga      60
232 cttctcaaga cgtcgtataa agtaaacaat gatataaatg atttatactt gcaattaact      120
W--> 233 attnaaatat agtaatatat atctttccgt gctaggtggg gaggtagcgg ttccctgtac      180
234 tcgaaatccg ctttatgcga ggcttaattc ctttgttgag gccgtatttt tgcgaagtct      240
235 gcccaaagca cgtagtgttt gaagatttcg gtcctt                                275

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VERIFICATION SUMMARY

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L:233 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8